1652

1600
#13/Raw
07.10.02

RAW SEQUENCE LISTING DATE: 06/10/2002
PATENT APPLICATION: US/09/903,770A TIME: 16:26:03

Input Set : A:\203979.txt
Output Set: N:\CRF3\06102002\I903770A.raw


```
 3 <110> APPLICANT: MOECKEL, BETTINA
 4       FARWICK, MIKE
 5       HERMANN, THOMAS
 6       KREUTZER, CAROLINE
 7       PFEFFERLE, WALTER
 9 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE lysR1 GENE
11 <130> FILE REFERENCE: 203979US
13 <140> CURRENT APPLICATION NUMBER: 09/903,770A
14 <141> CURRENT FILING DATE: 2001-07-13
16 <160> NUMBER OF SEQ ID NOS: 5
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1311
22 <212> TYPE: DNA
23 <213> ORGANISM: Corynebacterium glutamicum
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (201)...(1109)
28 <223> OTHER INFORMATION:
30 <400> SEQUENCE: 1
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33 gatagggcgg aacccatcac catcaacact gcagcggact gtttattcat gcccttgatt    120
35 attgccaaag aaacctttaa ggactagatc gaaaaacagc caactatagt taagtaatac    180
37 tgaacaattt tggaggtgtc gtg ctc aat ctc aac cgc tta cac atc ctg cag    233
38                         Val Leu Asn Leu Asn Arg Leu His Ile Leu Gln
39                         1               5                  10
41 gaa ttc cac cgc ctg gga acg att aca gca gtg gcg gaa tcc atg aac      281
42 Glu Phe His Arg Leu Gly Thr Ile Thr Ala Val Ala Glu Ser Met Asn
43             15                  20                  25
45 tac agc cgc tct gcc atc tcc caa caa atg gcg ctg ctg gaa aaa gaa      329
46 Tyr Ser Arg Ser Ala Ile Ser Gln Gln Met Ala Leu Leu Glu Lys Glu
47         30                  35                  40
49 att ggt gtg aaa ctc ttt gaa aaa agc ggc cga aac ctc tac ttc aca      377
50 Ile Gly Val Lys Leu Phe Glu Lys Ser Gly Arg Asn Leu Tyr Phe Thr
51     45                  50                  55
53 gaa caa ggc gaa gtg ttg gcc tca gaa aca cat gcg atc atg gca gca      425
54 Glu Gln Gly Glu Val Leu Ala Ser Glu Thr His Ala Ile Met Ala Ala
55 60                  65                  70                  75
57 gtc gac cat gcc cgc gca gcc gtt cta gat tcg ctg tct gaa gtg tcc      473
58 Val Asp His Ala Arg Ala Ala Val Leu Asp Ser Leu Ser Glu Val Ser
59                 80                  85                  90
61 gga acg ctg aaa gtc acc tcc ttc caa tcc ctg ctg ttc acc ctt gcc      521
62 Gly Thr Leu Lys Val Thr Ser Phe Gln Ser Leu Leu Phe Thr Leu Ala
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63              95                  100                 105
65 ccg aaa gcc atc gcg cgc ctg acc gag aaa tac cca cac ctg caa gta      569
66 Pro Lys Ala Ile Ala Arg Leu Thr Glu Lys Tyr Pro His Leu Gln Val
67          110                 115                 120
69 gaa atc tcc caa cta gaa gtc acc gca gcg ctc gaa gaa ctc cgc gcc      617
70 Glu Ile Ser Gln Leu Glu Val Thr Ala Ala Leu Glu Glu Leu Arg Ala
71      125                 130                 135
73 cgc cgc gtc gac gtc gca ctc ggc gag gaa tac ccc gtg gaa gtc ccc      665
74 Arg Arg Val Asp Val Ala Leu Gly Glu Glu Tyr Pro Val Glu Val Pro
75 140                 145                 150                 155
77 ctt gtt gag gcc agc att cac cgc gaa gtc ctc ttc gaa gac ccc atg      713
78 Leu Val Glu Ala Ser Ile His Arg Glu Val Leu Phe Glu Asp Pro Met
79                 160                 165                 170
81 ctg ctc gtc acc cca gca agc ggc cca tac tct ggc ctc acc ctg cca      761
82 Leu Leu Val Thr Pro Ala Ser Gly Pro Tyr Ser Gly Leu Thr Leu Pro
83              175                 180                 185
85 gaa ctc cgc gac atc ccc atc gcc atc gat cca ccc gac ctt ccc gcg      809
86 Glu Leu Arg Asp Ile Pro Ile Ala Ile Asp Pro Pro Asp Leu Pro Ala
87          190                 195                 200
89 ggc gaa tgg gtc cat agg ctc tgc cgg cgc gcc ggg ttt gag ccc cgc      857
90 Gly Glu Trp Val His Arg Leu Cys Arg Arg Ala Gly Phe Glu Pro Arg
91      205                 210                 215
93 gtg acc ttt gaa acc agc gat ccc atg ctc caa gca cac ctc gtg cgt      905
94 Val Thr Phe Glu Thr Ser Asp Pro Met Leu Gln Ala His Leu Val Arg
95 220                 225                 230                 235
97 agc ggc ttg gcc gtg aca ttt tcc ccc aca ctg ctc acc ccg atg ctg      953
98 Ser Gly Leu Ala Val Thr Phe Ser Pro Thr Leu Leu Thr Pro Met Leu
99                 240                 245                 250
101 gaa agc gtg cac atc cag ccg ctg ccc ggc aac ccc acg cgc acg ctc     1001
102 Glu Ser Val His Ile Gln Pro Leu Pro Gly Asn Pro Thr Arg Thr Leu
103             255                 260                 265
105 tac acc gcg gtc agg gaa ggg cgc cag ggg cat cca gcc att aaa gct     1049
106 Tyr Thr Ala Val Arg Glu Gly Arg Gln Gly His Pro Ala Ile Lys Ala
107         270                 275                 280
109 ttt cga cga gcc ctc gcc cat gtg gcc aaa gaa tct tat ttg gag gct     1097
110 Phe Arg Arg Ala Leu Ala His Val Ala Lys Glu Ser Tyr Leu Glu Ala
111     285                 290                 295
113 cgt cta gta gag tgagttcttg tgagccttca gacaaatcat cgcccagtac         1149
114 Arg Leu Val Glu
115 300
117 tcgtcgttga cttcggcgca cagtacgcgc agctgatcgc acgtcgtgtg cgtgaggccg   1209
119 gcatctactc cgaagtcatc ccgcacaccg ccaccgcaga cgatgtgcgc gctaaaaatg   1269
121 cagcagccct cgtcctttcc ggtggcccat cctccgtgta tg                     1311
124 <210> SEQ ID NO: 2
125 <211> LENGTH: 303
126 <212> TYPE: PRT
127 <213> ORGANISM: Corynebacterium glutamicum
129 <400> SEQUENCE: 2
131 Val Leu Asn Leu Asn Arg Leu His Ile Leu Gln Glu Phe His Arg Leu
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PATENT APPLICATION: US/09/903,770A TIME: 16:26:03

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132 1               5                   10                  15
135 Gly Thr Ile Thr Ala Val Ala Glu Ser Met Asn Tyr Ser Arg Ser Ala
136             20                  25                  30
139 Ile Ser Gln Gln Met Ala Leu Leu Glu Lys Glu Ile Gly Val Lys Leu
140         35                  40                  45
143 Phe Glu Lys Ser Gly Arg Asn Leu Tyr Phe Thr Glu Gln Gly Glu Val
144     50                  55                  60
147 Leu Ala Ser Glu Thr His Ala Ile Met Ala Ala Val Asp His Ala Arg
148 65                  70                  75                  80
151 Ala Ala Val Leu Asp Ser Leu Ser Glu Val Ser Gly Thr Leu Lys Val
152                 85                  90                  95
155 Thr Ser Phe Gln Ser Leu Leu Phe Thr Leu Ala Pro Lys Ala Ile Ala
156             100                 105                 110
159 Arg Leu Thr Glu Lys Tyr Pro His Leu Gln Val Glu Ile Ser Gln Leu
160         115                 120                 125
163 Glu Val Thr Ala Ala Leu Glu Glu Leu Arg Ala Arg Arg Val Asp Val
164     130                 135                 140
167 Ala Leu Gly Glu Glu Tyr Pro Val Glu Val Pro Leu Val Glu Ala Ser
168 145                 150                 155                 160
171 Ile His Arg Glu Val Leu Phe Glu Asp Pro Met Leu Leu Val Thr Pro
172                 165                 170                 175
175 Ala Ser Gly Pro Tyr Ser Gly Leu Thr Leu Pro Glu Leu Arg Asp Ile
176             180                 185                 190
179 Pro Ile Ala Ile Asp Pro Pro Asp Leu Pro Ala Gly Glu Trp Val His
180         195                 200                 205
183 Arg Leu Cys Arg Arg Ala Gly Phe Glu Pro Arg Val Thr Phe Glu Thr
184     210                 215                 220
187 Ser Asp Pro Met Leu Gln Ala His Leu Val Arg Ser Gly Leu Ala Val
188 225                 230                 235                 240
191 Thr Phe Ser Pro Thr Leu Leu Thr Pro Met Leu Glu Ser Val His Ile
192                 245                 250                 255
195 Gln Pro Leu Pro Gly Asn Pro Thr Arg Thr Leu Tyr Thr Ala Val Arg
196             260                 265                 270
199 Glu Gly Arg Gln Gly His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu
200         275                 280                 285
203 Ala His Val Ala Lys Glu Ser Tyr Leu Glu Ala Arg Leu Val Glu
204     290                 295                 300
207 <210> SEQ ID NO: 3
208 <211> LENGTH: 383
209 <212> TYPE: DNA
210 <213> ORGANISM: Corynebacterium glutamicum
212 <400> SEQUENCE: 3
213 ttccaatccc tgctgttcac ccttgccccg aaagccatcg cgcgcctgac cgagaaatac     60
215 ccacacctgc aagtagaaat ctcccaacta gaagtcaccg cagcgctcga agaactccgc    120
217 gcccgccgcg tcgacgtcgc actcggcgag gaataccccg tggaagtccc ccttgttgag    180
219 gccagcattc accgcgaagt cctcttcgaa gaccccatgc tgctcgtcac cccagcaagc    240
221 ggcccatact ctggcctcac cctgccagaa ctccgcgaca tccccatcgc catcgatcca    300
223 cccgaccttc ccgcgggcga atgggtccat aggctctgcc ggcgcgccgg gtttgagccc    360
225 cgcgtgacct ttgaaaccag cga                                           383
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RAW SEQUENCE LISTING DATE: 06/10/2002
PATENT APPLICATION: US/09/903,770A TIME: 16:26:04

Input Set : A:\203979.txt
Output Set: N:\CRF3\06102002\I903770A.raw

228 <210> SEQ ID NO: 4
229 <211> LENGTH: 20
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: synthetic DNA
236 <400> SEQUENCE: 4
237 ttccaatccc tgctgttcac 20
240 <210> SEQ ID NO: 5
241 <211> LENGTH: 20
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: synthetic DNA
248 <400> SEQUENCE: 5
249 gtgacctttg aaaccagcga 20

VERIFICATION SUMMARY DATE: 06/10/2002
PATENT APPLICATION: US/09/903,770A TIME: 16:26:05

Input Set : A:\203979.txt
Output Set: N:\CRF3\06102002\I903770A.raw